Antimicrobial Resistance and ERIC PCR Patterns of Shigella sonnei Strains Isolated from Pediatric Patients in Tehran, Iran (2008-2010)

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Background & Objectives: *Shigella sonnei* is considered as a major cause of diarrheal disease in both developing and developed countries. Iran is one of the endemic areas of shigellosis. The present study was undertaken to investigate the antibiotic susceptibility and genetic relatedness of S. sonnei strains isolated from pediatric patients in Tehran, Iran.

Methods: The study included all *S. sonnei* strains isolated from pediatric patients with diarrhea who were admitted to several hospitals in Tehran, Iran, during 2008-2010. Shigella spp. strains were recovered from patients using standard microbiological methods. *S. sonnei* strains were further studied by antimicrobial susceptibility testing and Enterobacterial Repetitive Intergenic Consensus (ERIC) - PCR analysis.

Results: Eighty nine Shigella isolates were isolated. *S. sonnei* was themost prevalent Shigella species (60.7%) followed by, *S. flexneri* (31.5%). Eleven antimicrobial resistance patterns (R1-R11) were identified among S. sonnei isolates. The majority of the strains were resistant to trimethoprim-sulfamethoxazole, tetracycline and streptomycin. All isolates were susceptible to ciprofloxacin, ceftizoxime and chloramphenicol. All strains were typable by ERIC-PCR. Five ERIC-PCR patterns (E1-E5) were found among *S. sonnei* isolates; however the half of the isolates was clustered in E4 pattern.

Conclusion: We found the antibiotic resistance rates are increasing among *S. sonnei* strains. As reported in recent previous studies, our finding also indicated that a predominant clone or limited clones of *S. sonnei* are responsible for shigellosis caused by this Shigella species in pediatric patients in Tehran, Iran.

Keywords: *Shigella sonnei*; Antibiotic Resistance; ERIC-PCR